

### **THE REMARKS**

Claims 1, 4, 5, 7-9, 13-16, 19, and 21-27 were pending prior to entering the amendments.

#### **The Amendments**

Claim 1 is amended to clarify the meaning of the claim. The amendment of Claim 1 is supported by Publication 2005-0095605 at Paragraphs [0014], [108], [109], [0154], [158] and Figure 3.

The amendments of FIGURES 3-2 and 3-3 are to insert the bold "H". A marked-up copy is attached herewith to show the changes made. At Paragraph [0098], the application describes that FIGURES 3-1 to 3-8 depict an alignment of the amino acid sequences of 81 natural proteorhodopsin variants. The bold "H" indicates the position of a conserved histidine, which corresponds to H75 of Bac31A8. Applicants inadvertently omitted the labeling of "H" in FIGURES 3-2 to 3-3 as filed, and are submitting herewith replacement FIGURES 3-1 to 3-8 to insert the bold "H". Support for the amendment can be found in Figure 2-2 of the Provisional Application No. 60/429,518, which is incorporated by reference under § 1.57(a). Support for the amendment can also be found in Paragraph [0098] of the instant application, where it describes that the bold "H" corresponds to H75 of Bac31A8. In Figures 3-1, because of the 6-amino acid gap in the alignment of BAC31A8, the conserved H is shown at position 81, which is the 75<sup>th</sup> amino acid.

No new matter is added in the amendments. The Examiner is requested to enter the amendments.

#### **Restriction Requirement**

The key of this invention is that Applicant has discovered that a mutation in the conserved histidine of a naturally occurring proteorhodopsin provides a proteorhodopsin mutant with improved optical characteristics, i.e. has lower  $pK_{th}$  in comparison with the naturally occurring proteorhodopsin. Such technical feature was not taught or disclosed in any prior art.

The Examiner found Applicants' arguments unpersuasive because the phrase "conserved histidine" was unclear. Applicants have amended Claim 1 to clarify the meaning of the claim. In

view of the claim amendment and the filing of RCE, Applicants respectfully request that the Examiner reconsiders the restriction requirement.

### **35 U.S.C. 112, Second Paragraph Rejection**

Claims 1, 4-5, 7-9, 14, 23-27 remain rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The rejection is overcome in view of the claim amendment.

### **Conserved histidine residue**

The Examiner states that the phrase "conserved histidine residue" in claim 1 (and its dependent claims 4-5, 7-8, 14) is unclear. Applicants have amended the claim to recite that the conserved histidine is present at the position equivalent to position 75 of SEQ ID NO: 3 when the proteorhodopsin variant is aligned with SEQ ID NO: 3 for a maximum identity.

At Paragraph [0014], the application describes that a conserved histidine residue is at, for example, amino acid position 75 of Bac31A8, or position 77 of Hot75m1, or its equivalent position of a proteorhodopsin variant.

At Paragraph [0154], the application describes methods known in the art for aligning protein sequences. There can be deletions or insertions when two structures are aligned for maximum identity. For example, proteorhodopsin Bac31A8 has only 249 amino acids while proteorhodopsin Hot75m1 has 252 amino acids. Aligning the two sequences shows that Bac31A8 has no residue corresponding to 214 of Hot75M1. Thus, the amino acid sequence of Bac31A8 would appear very different from Hot75m1 unless a gap is recorded between locations 211 and 212 of Bac31A8 (see FIG. 2 for alignment).

As shown in Figure 3, naturally occurring proteorhodopsins have high degree of homology. Applicants have shown "the conserved histidine" in 81 naturally occurring proteorhodopsins. **In the 81 proteorhodopsin sequences shown in Figures 3-1 to 3-8, 57 of them contain only one histidine residue, which is the conserved histidine residue.** The remaining 24 proteorhodopsins (HOT2C02, HOT75m3, medA15\_R8\_3, medA15\_r8ex7, medA15\_R8ex9, medA15\_r9\_3, medA15r10b5, medA15r11b3, medA15r8b3, medA15r8b8,

medA15r8b9, medA15r8ex4, medA15r9b5, medA15r9b7, medA17\_r8\_11, medA17\_r8\_15, medA17\_R8\_6, medA17R9\_1, medA19\_R8\_16, medA19\_R8\_19, medA19\_R8\_20, medA19\_r9\_9, PalB1, and PalE6) contain two histidine residues.

There are only very few histidine residues in the naturally occurring proteorhodopsins, as illustrated in Figures 3-1 to 3-8. **A skilled person in the art can easily compare and align the amino acid sequences of Bac31A8 and any naturally occurring proteorhodopsin or its proteorhodopsin homolog having 90% identity and determine where the conserved histidine is.**

Therefore, the phrase “the conserved histidine” in a naturally occurring proteorhodopsin is not indefinite.

#### **Having at least 90% identity**

The Examiner states that the phrase "having at least 90% identity" in claim is unclear. Applicants have amended Claim 1 to recite the proteorhodopsin mutant is a proteorhodopsin variant comprising a mutation in a conserved histidine residue, said proteorhodopsin variant is a naturally occurring proteorhodopsin or a proteorhodopsin homolog having at least 90% identity with the naturally occurring proteorhodopsin.

Paragraph [0003] describes that proteorhodopsins are integral membrane proteins isolated from uncultivated marine eubacteria and function as light-driven proton pumps. The naturally occurring proteorhodopsin in Claim 1 is meant to include naturally occurring proteorhodopsins isolated from marine eubacteria.

Paragraph [0154] describes that closeness of relation can be measured by comparing amino-acid sequences. Methods of aligning protein sequences and methods of defining relatedness are described in the application and well known to a person skilled in the art. A skilled person can easily align a naturally occurring proteorhodopsin with its homolog and compare them for percent of identity.

Therefore, the phrase “having at least 90% identity” is not indefinite.

### **35 U.S.C. 112, First Paragraph Rejection**

Claims 1, 4-5, 7-9, 14, 23-27 are rejected under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the written description requirement.

Contrary to what the Examiner has asserted, Applicants did not claim 90% homologs of a homolog. However, to further the prosecution, Applicants have amended the claims to clarify the meaning of the claims.

Naturally occurring proteorhodopsins have known and defined amino acid sequences. Naturally occurring proteorhodopsins have similar amino acid sequences as illustrated by the 81 sequences in Figure 3. Figure 3 also shows the amino acid sequence alignment of 81 naturally occurring proteorhodopsins and the conserved histidine residue. It is not possible for Applicant to list the amino acid sequences of all naturally occurring proteorhodopsins and show the alignments of the sequences to demonstrate the conserved histidine. However, **Applicant has provided a large representative number (81) of species.**

A proteorhodopsin homolog having at least 90% identity with a naturally occurring proteorhodopsin can be made by changing several amino acids of a naturally occurring proteorhodopsin, and testing its ability for undergoing a photocycle containing an "M-state" or "M-like state" (see Paragraph [0108]). This can be easily done by a person skilled in the art.

Therefore, 35 U.S.C. §112, first paragraph of Claims 1, 4-5, 7-9, 14, 23-27 should be withdrawn.

### **35 U.S.C. 102(e) Rejection**

Claims 1, 25-27 remain rejected under 35 U.S.C. §102(e) as allegedly being anticipated by La Rosa et al (US2007/0192889).

La Rosa et al. disclose a plant protein that only shows 7.6% sequence identity with the entire sequence of SEQ ID NO: 3, and 22.4% sequence similarity in a short stretch. When the sequence of the La Rosa protein is aligned and compared with the 81 naturally occurring proteorhodopsins in Figure 3, it is clear that the La Rosa protein is **not** a proteorhodopsin variant comprising a mutation in a conserved histidine residue, wherein said proteorhodopsin variant is a naturally occurring proteorhodopsin or a proteorhodopsin homolog having at least 90% identity with the naturally occurring proteorhodopsin.

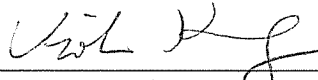
Therefore, the 102(e) rejection of Claims 1, and 25-27 over La Rosa et al should be withdrawn.

**CONCLUSION**

Applicants believe that the application is now in good and proper condition for allowance. Early notification of allowance is earnestly solicited.

Date: June 2, 2008

Respectfully submitted,



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|            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|
| Pale7      | TMGKLLLILG | SAIALPSFAA | AGGD....LD | ISDTVGVSFW | LVTAGMLAAT |
| RED19      | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| RED2       | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| RED23      | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| RED27      | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| RED30      | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| RED4       | .MGKLLRLG  | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| RED5       | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDA9      | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDB9      | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDF9      | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDr6a5a14 | .MGKLLLILG | SVIALPTFAA | GGGD....PD | ASDYGVSFW  | LVTALLAST  |
| REDr6a5a6  | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDr7_1_15 | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASGYTGVSFW | LVTALLAST  |
| REDr7_1_16 | .MGKRLVILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDr7_1_4  | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDs3_15   | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| REDs3_7    | .MGKLLLILG | SVIALPTFAA | GGGD....LD | ASDYGVSFW  | LVTALLAST  |
| ANT32C12   | ..MKLLLILG | SAIALPSFAA | AGGD....LD | ISDTVGVSFW | LVTAGMLAAT |
| HOT2C02    | .....      | ....MKVLM  | NPGD.....  | ...HVAISFW | LISMAMVAAT |

|              |            |           |   |       |      |
|--------------|------------|-----------|---|-------|------|
|              | 51         |           |   | H     | 100  |
| BAC31A8      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| BAC40E8      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| BAC64A5      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| HOT0m1       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| HOT75m1      | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| HOT75m3      | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| HOT75m4      | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| HOT75m8      | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| MB0m1        | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB0m2        | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB100m10     | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB100m5      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB100m7      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB100m9      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB20m12      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB20m2       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB20m5       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB40m1       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB40m12      | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MB40m5       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED101       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED102       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED106       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED202       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED204       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED208       | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED25        | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED26        | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED27        | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| MED36        | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| medA15_r8_1  | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| medA15_r8_3  | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| medA15_r8ex7 | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| medA15_r8ex9 | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| medA15_r9_3  | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| medA15r10b5  | VFFFVERDQV | SAKWKTSLT | V | ETGDS | .... |
| medA15r11b3  | VFFFIERDRV | SAKWKTSLT | V | ETGDS | .... |
| medA15r11b9  | VFFFVERDRV | SAKWKTSLT | V | ETGDS | .... |
| medA15r8b3   | VFFFIERDRV | SAKWKTSLT | V | ETGDS | .... |
| medA15r8b8   | VFFFIERDRV | SAKWKTSLT | V | ETGDS | .... |
| medA15r8b9   | VFFFIERDRV | SAKWKTSLT | V | ETGDS | .... |

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Figure 3-2

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|              |             |            |            |            |             |
|--------------|-------------|------------|------------|------------|-------------|
| medA15r8ex4  | VFFFIVERDRV | SSKWKTSLTV | SALVTLIAAV | HYFYMRDVVW | ATGESP....  |
| medA15r8ex6  | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| medA15r9b5   | VFFFVERDRV  | AAKWKTSLTV | SGLVTGIAFW | HYMYMRGVVW | ETGESP....  |
| medA15r9b7   | VFFFVERDQV  | SAKWKTSLTV | SGLVTGIAFW | HYLYMRGVWI | ETGETP....  |
| medA17_r8_11 | VFFFIVERDRV | SAKWKTSLTV | SALVTLIAAV | HYFYMRDVVW | ATGESP....  |
| medA17_r8_15 | VFFFIVERDRV | SAKWKTSLTV | SALMTLIAAV | HYFYMRDVVW | ATGESP....  |
| medA17_R8_6  | VFFFVERDQV  | SAKWKTSLTV | SGLVTGIAFW | HYLYMRGVVW | ETGDSP....  |
| medA17R9_1   | VFFFIERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYLYMRGVVW | DSWNPETGMG  |
| medA19_R8_16 | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGGSP....  |
| medA19_R8_19 | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGGSP....  |
| medA19_R8_20 | VFFFVERDQV  | SAKWKTSLTV | SGLVTGIAFW | HYLYMRGVWI | ETGETP....  |
| medA19_r9_9  | VFFFVERDQV  | SAKWKTSLTV | SGLVTGIAFW | HYLYMRGVWI | ETGETP....  |
| PalB1        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalB2        | VFFFVERDQV  | SAEWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalB5        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalB6        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalB7        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalB8        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalE1        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalB6        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| PalE7        | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| RED19        | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| RED2         | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| RED23        | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| RED27        | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| RED30        | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGSSP....  |
| RED4         | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| RED5         | VFFFVERDRV  | SAKWKTSLAV | SGLITGIAFW | HYMYMRGVWI | ETGDSP....  |
| REDA9        | VFFFVERDRV  | SAKWKTSLAV | SGLITGIAFW | HCMYMRGVWI | ETGDSP....  |
| REDB9        | VFSFVERDRV  | SAKWKTSLTV | SGLITGIAFW | HYMYMRGVWI | ETGDSP....  |
| REDF9        | VFFFVERDRV  | SAKWKTSLTV | SGLITGIAFW | HYMYMRGVWI | ETGDSP....  |
| REDr6a5a14   | VFFFVERDRV  | SAEWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| REDr6a5a6    | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| REDr7_1_15   | VFFFVERDRV  | SAKWKTSLTV | PGLITDIAFW | HYMYMRGVWI | ETGDSP....  |
| REDr7_1_16   | VFFFVERDRV  | SAKWKTSLTV | SGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| REDr7_1_4    | VFFFVERDRV  | SAKWKTSLTV | PGLITDIAFW | HYMYMRGVWI | ETGDSP....  |
| REDS3_15     | VFFFVERDRV  | SAKWKTSLTV | PGLVTGIAFW | HYMYMRGVWI | ETGDSP....  |
| REDS3_7      | VFFFVERDRV  | SAKWKTSLTV | PGLITDIAFW | HYMYMRGVWI | ETGDSP....  |
| ANT32C12     | VFFFVERDQV  | SAKWKTSLTV | SGLITGIAFW | HYLYMRGVWI | DTGDTTP.... |
| HOT2C02      | AFFFLERDRV  | AAKWKTSLTV | AGLVTGIAAW | HYFYMRGVVW | ATGDSP....  |

|          |            |            |                                  |
|----------|------------|------------|----------------------------------|
|          | 101        |            | 150                              |
| BAC31A8  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| BAC40E8  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAAGLFKKL LVGSLVMLVF |
| BAC64A5  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| HOT0m1   | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAAGLFKKL LVGSLVMLVF |
| HOT75m1  | ...TVFRYID | WLLTVPLQMV | EFYLILAACT SVAASLFKKL LAGSLVMLGA |
| HOT75m3  | ...TVFRYID | WLLTVPLQMV | EFYLILAACT SVAASLFKKL LAGSLVMLGA |
| HOT75m4  | ...TVFRYID | WLLTVPLQVV | EFYLILAACT SVAASLFKKL LAGSLVMLGA |
| HOT75m8  | ...TVFRYID | WLLTVPLQMV | EFYLILAACT NVAASLFKKL LAGSLVMLGA |
| MB0m1    | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAAGLFKKL LVGSLVMLVF |
| MB0m2    | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAAGLFKKL LVGSLVMLVF |
| MB100m10 | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| MB100m5  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| MB100m7  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| MB100m9  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| MB20m12  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAA NVAGSLFKKL LVGSLVMLVF |
| MB20m2   | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAAGLFKKL LVGSLVMLVF |
| MB20m5   | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| MB40m1   | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| MB40m12  | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |
| MB40m5   | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAAGLFKKL LVGSLVMLVF |
| MED101   | ...TVFRYID | WLLTVPLLIC | EFYLILAAAT NVAGSLFKKL LVGSLVMLVF |

Figure 3-3